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A. CTTATCGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCAT  
CACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCA  
+++++ ↑ ++++++  
ATGTATCTTATCATGTC CLEAVAGE SITE

B.  AAUAAA  
+++++ GCA

C.  GCAaaaaaaaaaaaaaaaaaaaaaa

+ UPSTREAM AND DOWNSTREAM  
CLEAVAGE-POLYADENYLATION ELEMENTS

Fig. 1



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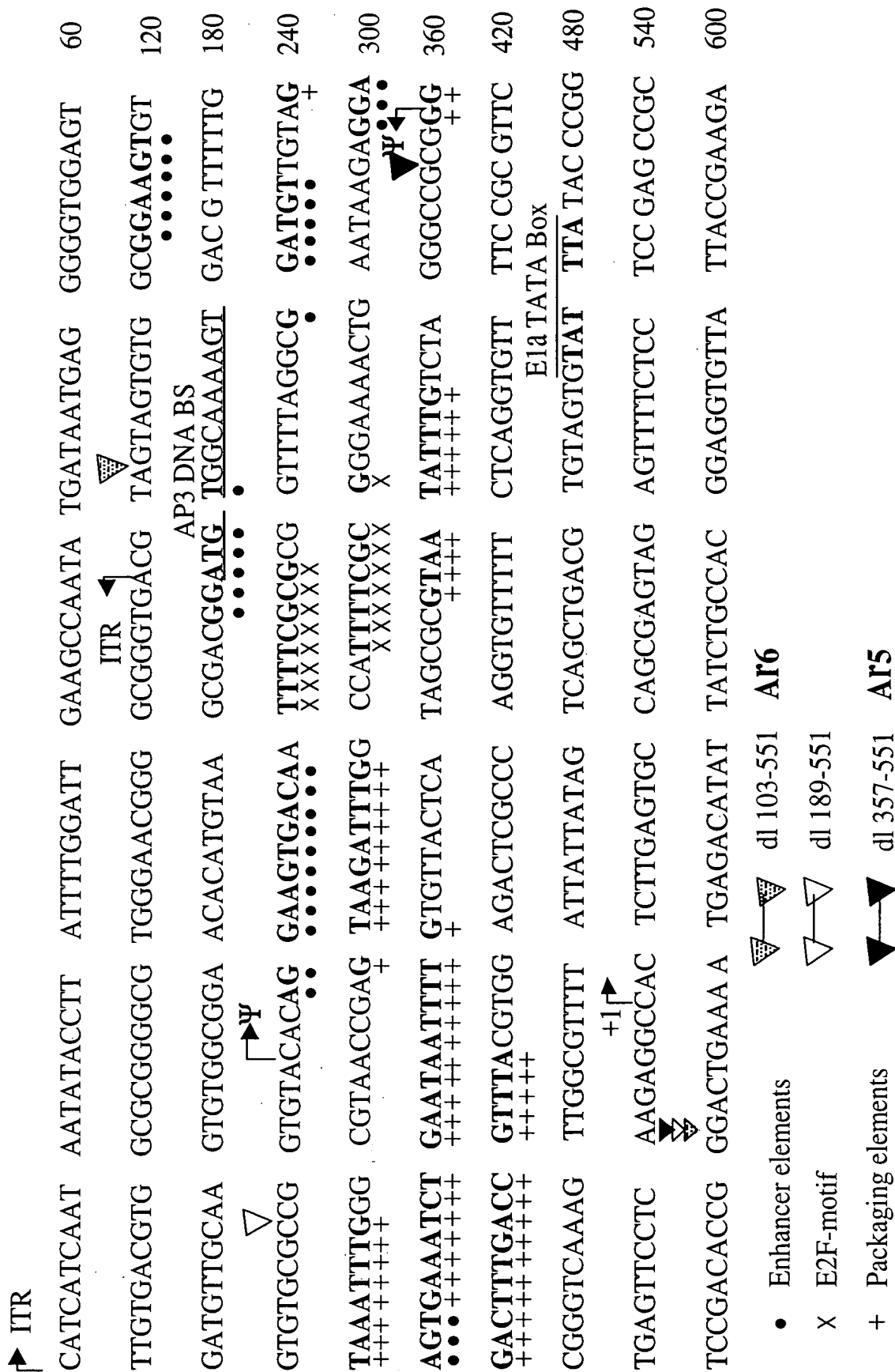


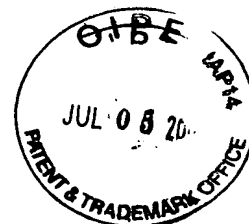
Fig. 2



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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT  
+-----ITR-----  
61 TTGTGACGTGGCGCGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT  
+-----ITR-----+ +---  
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC  
-----polyA-----  
181 ACAAATTTACAAATAAAGCATTTTTTTCACCTGCATTCTAGTTGTGGTTTGTCCAACTC  
-----polyA-----  
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATCATCCGGACAAAGCCTGC  
-----+ +-----  
301 GCGCGCCCCGCCCCGCCATTGGCCGTACCGCCCCGCGCCGCGCCCCATCTCGCCCCCTCG  
-----E2F-1 PROMOTER-----  
361 CCGCCGGGTCCGGCGCGTTAAAGCCAATAGGAACCGCCGCGTGTTCCTCGTCACGGCCG  
-----E2F-1 PROMOTER-----  
421 GGGCAGCCAATTGTGGCGGCGCTCGGCGGCTCGTGGCTCTTTTCGCGGCAAAAAGGATTTG  
-----E2f-1 PROMOTER-----  
481 GCGCGTAAAAGTGGCCGGGACTTTGCAGGCAGCGGCGGGGGCGGAGCGGGATCGAG  
-----E2f-1 PROMOTER-----  
541 CCCTCGATGATATCAGATCATCGGATCCCGGTCTGACTGAAAATGAGACATATTATCTGCC  
-----+ +-----  
601 ACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGG  
-----E1a GENE-----  
661 TACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAACTGT  
-----E1a GENE-----  
721 ATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTTC  
-----E1a GENE-----  
781 CCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGC  
-----E1a GENE-----  
841 CCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCT  
-----E1a GENE-----

Fig. 3A



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901 TGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGG  
-----E1a GENE-----

961 CTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATG  
-----E1a GENE-----

1021 TGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCAATTATCACCGGAGGAATACGGGGGACC  
-----E1a GENE-----

1081 CAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGCATGTTTGTCTACAGTAAGT  
-----E1a GENE-----

1141 GAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTGTGGTAATTTTTTTTTTAAT  
-----E1a GENE-----

1201 TTTTACAGTTTGTGGTTTAAAGAATTTTGTATTGTGATTTTTTTTAAAGGTCCTGTGTC  
-----E1a GENE-----

1261 TGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAAGACCTACCCGCCGTCTCTAA  
-----E1a GENE-----

1321 AATGGCGCCTGCTATCCTGAGACGCCCCGACATCACCTGTGTCTAGAGAATGCAATAGTAG  
-----E1a GENE-----

1381 TACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTGAGATACACCCGGTGGTCCC  
-----E1a GENE-----

1441 GCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGCGTCGCCAGGCTGTGGAATG  
-----E1a GENE-----

1501 TATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACTTGAGCTGTAAACGCCCCAG  
-----E1a GENE-----

1561 GCCATAAGGTGTAAACCTGTGATTGCGTGTGTGGTTAACGCCTTTGTTTGCTGAATGAGT  
-----E1a GENE-----

1621 TGATGTAAGTTTAATAAAGGGTGAGATAATGTTTAACTTGCATGGCGTGTTAAATGGGGC  
-----+-----

1681 GGGGCTTAAAGGGTATATAATGCGCCGTGGGCTAATCTTGGTTACATCTGACCTCATGGA  
-----E1b GENE-----

1741 GGCTTGGGAGTGTTTGAAGATTTTTCTGCTGTGCGTAACTTGCTGGAACAGAGCTCTAA  
-----E1b GENE-----

1801 CA  
--

Fig. 3B



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33881 AACCTACGCCCAGAAACGAAAGCCAAAAACCCACAACCTTCCTCAAATCGTCACTTCCGT  
33941 TTTCCCACGTTACGTCACTTCCCATTTTTAATTAAGAATTCTACAATTCCCAACACATACA  
34001 AGTTACTCCGCCCTAAAACCCTGGGCGAGTCTCCACGTAAACGGTCAAAGTCCCCGCGGC  
+-- PACKAGING SIGNAL-----  
34061 CCTAGACAAATATTACGCGCTATGAGTAACACAAAATTATTCAGATTTCACTTCCTCTTA  
-----PACKAGING SIGNAL-----  
34121 TTCAGTTTTCCCGCGAAAATGGCCAAATCTTACTCGGTTACGCCCAAATTTACTACAACA  
-----PACKAGING SIGNAL-----  
34181 TCCGCCTAAAACCGCGCGAAAATTGTCACTTCCTGTGTACACCGGCGCACACCAAAAACG  
-----+  
34241 TCACTTTTGCCACATCCGTCGCTTACATGTGTTCCGCCACACTTGCAACATCACACTTCC  
34301 GCCACACTACTACGTCACCCGCCCCGTTCCCACGCCCCGCGCCACGTCACAAACTCCACC  
+-----ITR-----  
34361 CCCTCATTATCATATTGGCTTCAATCCAAAATAAGGTATATTATTGATGATG  
-----ITR-----+

Fig. 3C



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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT  
----- ITR -----  
61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGCCGCTAGCGAT  
----- ITR ----- ++ --- MCS -----  
121 ATCGGATCCCGGTCTGACTGAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGA  
----- E1a -----  
181 AGAAATGGCCGCCAGTCTTTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCC  
----- E1a -----  
241 ACCTCCTAGCCATTTTGAACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGC  
----- E1a -----  
301 CCCCGAAGATCCCAACGAGGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGC  
----- E1a -----  
361 GGTGCAGGAAGGGATTGACTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCC  
----- E1a -----  
421 TCACCTTTCCCGGCAGCCCGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCC  
----- E1a -----  
481 AAACCTTGTACCGGAGGTGATCGATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGA  
----- E1a -----  
541 CGACGAGGATGAAGAGGGTGAGGAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGG  
----- E1a -----  
601 TTGCAGGTCTTGTCATTATCACCGGAGGAATACGGGGGACCCAGATATTATGTGTTTCGCT  
----- E1a -----

Fig. 4



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1 CATCATCAATAATATACCTTATTTTGGATTGAAGCCAATATGATAATGAGGGGGTGGAGT
+-----ITR-----
61 TTGTGACGTGGCGCGGGGCGTGGGAACGGGGCGGGTGACGTAGGGCGCGATCAAGCTTAT
-----ITR-----+ +-----
121 CGATACCGTCGAAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATC
-----polyA-----
181 ACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
-----polyA-----
241 ATCAATGTATCTTATCATGTCTGGATCCGCGCCGCTAGCGATATCGGATCCCGGTGCGACT
-----+ +-----
301 GAAAATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCT
-----E1a-----
361 TTTGGACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGA
-----E1a-----
421 ACCACCTACCCTTCACGAAGTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGA
-----E1a-----
481 GGAGGCGGTTTCGCAGATTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGA
-----E1a-----
541 CTTACTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCC
-----E1a-----
601 CGAGCAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGT
-----E1a-----
```

Fig. 5



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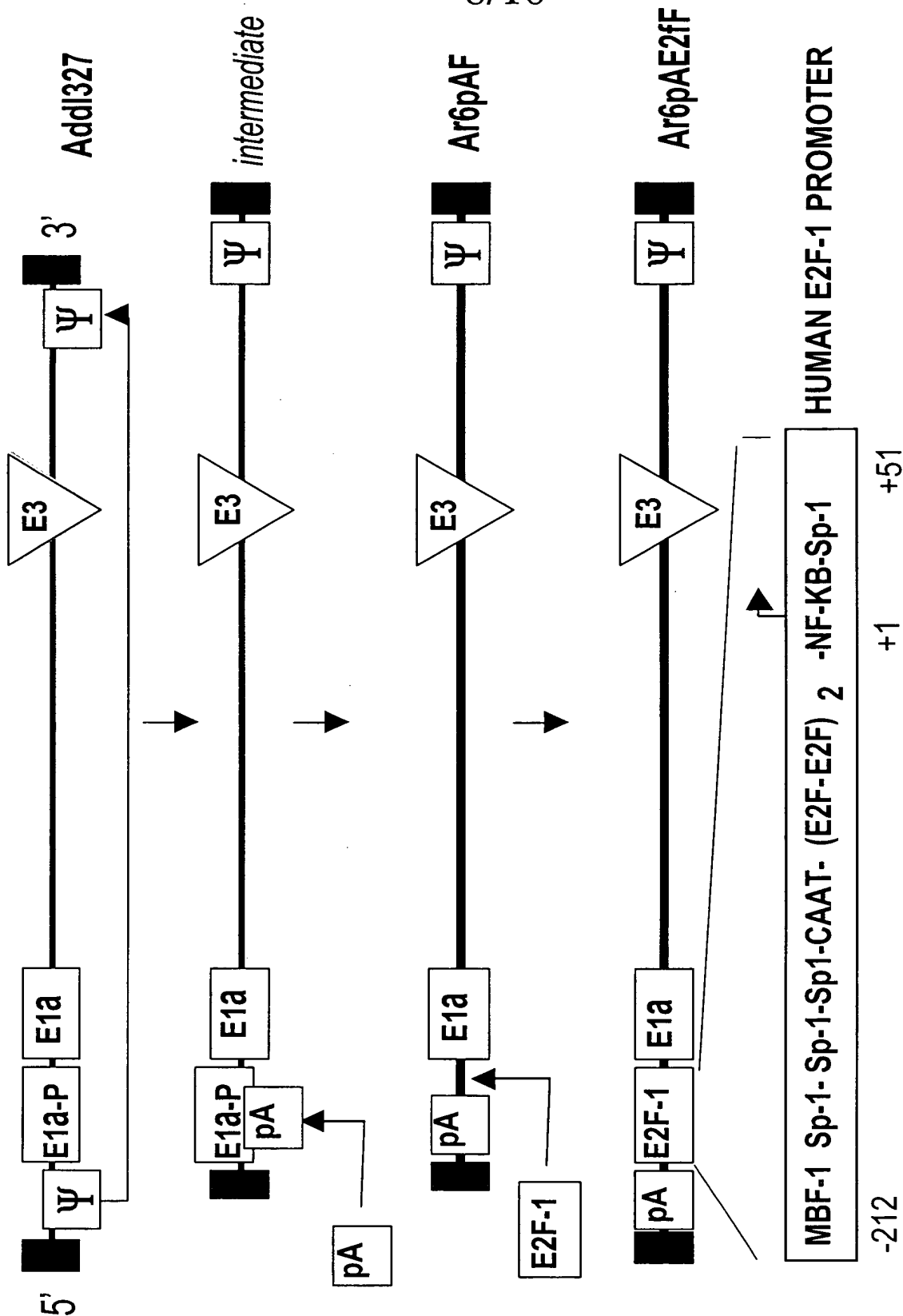


Fig. 6





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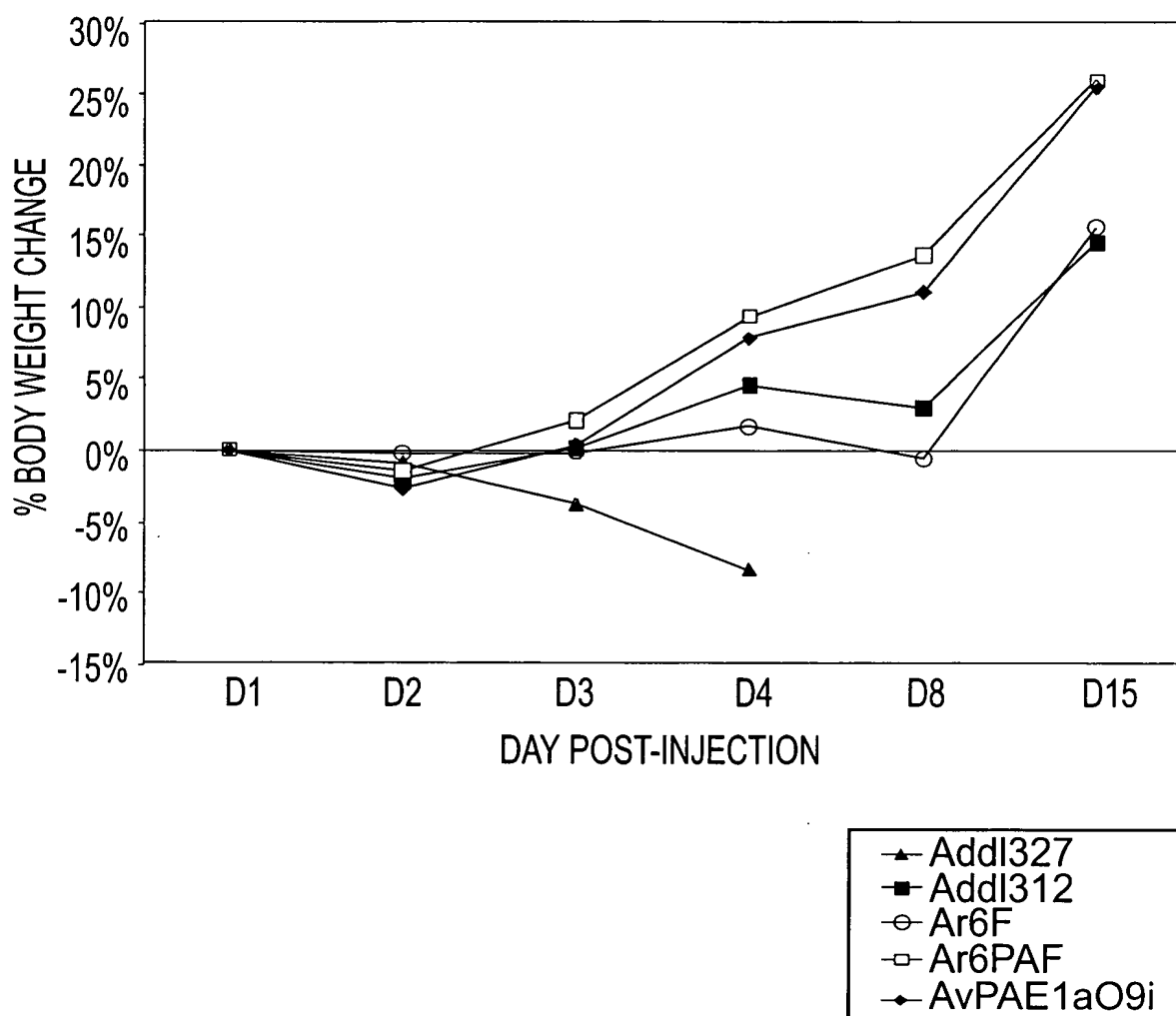


Fig. 7



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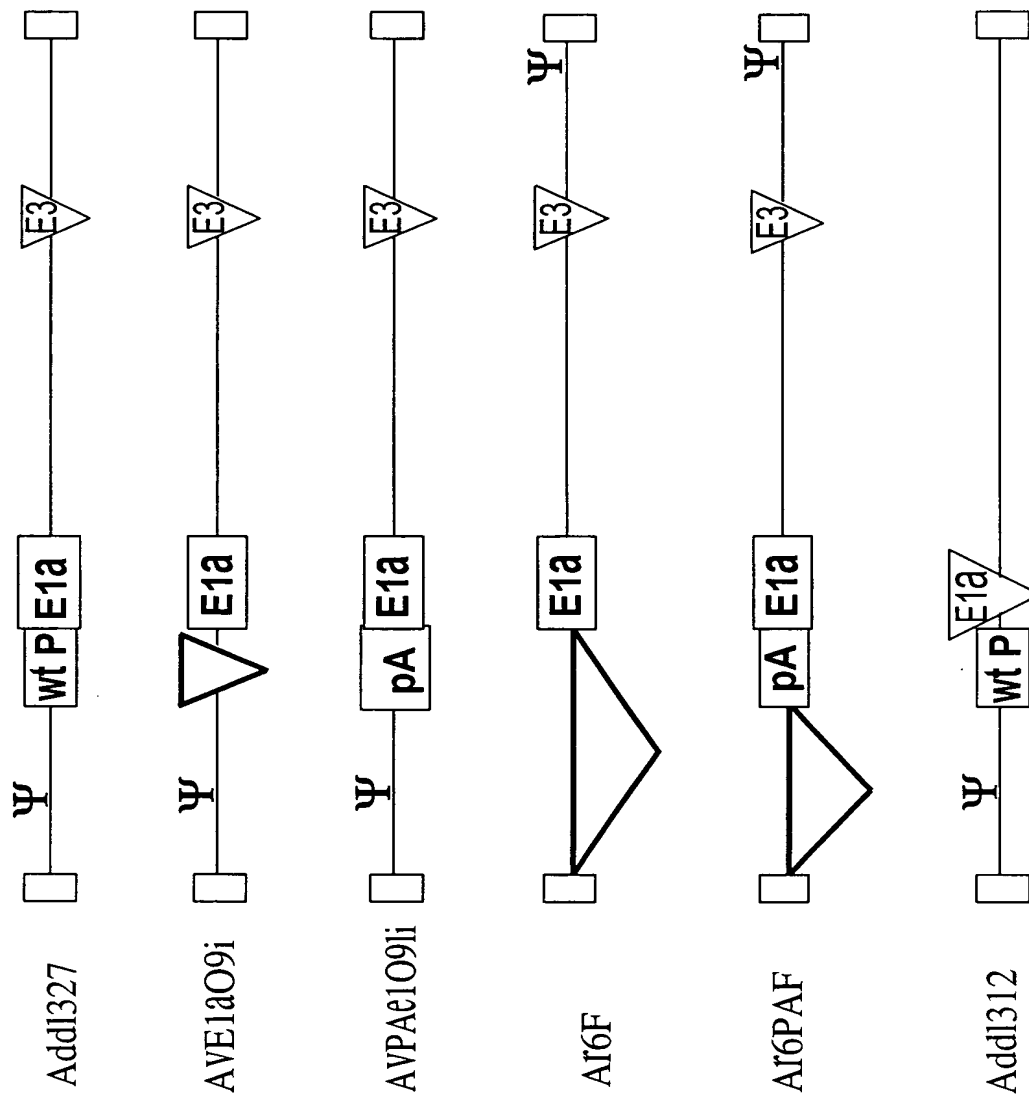


Fig. 8